

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(I) APPLICANT: NAKAMURA, SEIJI
SAKURAI, TAKASHI
NEZU, JUNI-ICHI

(ii) TITLE OF INVENTION: GENE ENCODING ADSEVERIN

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP
(B) STREET: P.O. Box 747
(C) CITY: Falls Church
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22040-0747

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: MURPHY Jr., Gerald M.
(B) REGISTRATION NUMBER: 28,977
(C) REFERENCE/DOCKET NUMBER: 230-110P

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (703) 205-8000
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Leu Thr Asn Asp Leu Thr Ala Gln
1 5

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Ile Thr Asn Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 27..2171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGCCGGAAC ATCGCGTGCC CGAGTC ATG GCC CAG GGG CTG TAC CAC GAG GAG
Met Ala Gln Gly Leu Tyr His Glu Glu
1 5

53

TTC GCC CGC GCG GGC AAG CGG GCG GGG CTG CAG GTC TGG AGA ATT GAG

101

Phe Ala Arg Ala Gly Lys Arg Ala Gly Leu Gln Val Trp Arg Ile Glu	25	
10 15 20		
AAG CTG GAG CTG GTG CCG GTG CCC GAG AGC GCG TAT GGC AAC TTC TAC	149	
Lys Leu Glu Leu Val Pro Val Pro Glu Ser Ala Tyr Gly Asn Phe Tyr		
30 35 40		
GTC GGG GAT GCC TAC CTG GTG CTC CAC ACG ACG CAG GCC AGC CGG GGC	197	
Val Gly Asp Ala Tyr Leu Val Leu His Thr Thr Gln Ala Ser Arg Gly		
45 50 55		
TTC ACC TAC CGC CTG CAC TTC TGG CTG GGA AAG GAG TGT ACT CAG GAT	245	
Phe Thr Tyr Arg Leu His Phe Trp Leu Gly Lys Glu Cys Thr Gln Asp		
60 65 70		
GAA AGC ACA GCA GCT GCC ATC TTT ACT GTT CAG ATG GAT GAC TAT TTG	293	
Glu Ser Thr Ala Ala Ile Phe Thr Val Gln Met Asp Asp Tyr Leu		
75 80 85		
GGT GGC AAA CCT GTG CAG AAC AGA GAA CTT CAA GGC TAT GAG TCT ACG	341	
Gly Gly Lys Pro Val Gln Asn Arg Glu Leu Gln Gly Tyr Glu Ser Thr		
90 95 100 105		
GAT TTT GTT GGC TAC TTT AAA GGA GGT CTG AAA TAC AAG GCT GGC GGT	389	
Asp Phe Val Gly Tyr Phe Lys Gly Gly Leu Lys Tyr Lys Ala Gly Gly		
110 115 120		
GTG GCG TCT GGA CTC AAT CAT GTG CTT ACA AAT GAC TTG ACT GCT CAG	437	
Val Ala Ser Gly Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Gln		
125 130 135		
AGG CTC CTG CAT GTG AAA GGT CGG AGA GTC GTC AGG GCC ACG GAA GTT	485	
Arg. Leu Leu His Val Lys Gly Arg Arg Val Val Arg Ala Thr Glu Val		
140 145 150		
CCC CTA AGC TGG GAC AGT TTC AAC AAG GGT GAC TGC TTC ATC ATT GAC	533	
Pro Leu Ser Trp Asp Ser Phe Asn Lys Gly Asp Cys Phe Ile Ile Asp		
155 160 165		
CTT GGC ACT GAA ATT TAC CAG TGG TGT GGA TCT TCT TGC AAC AAG TAC	581	
Leu Gly Thr Glu Ile Tyr Gln Trp Cys Gly Ser Ser Cys Asn Lys Tyr		
170 175 180 185		
GAG CGC CTG AAG GCC AGC CAG GTT GCC ATC GGC ATT CGG GAC AAT GAA	629	
Glu Arg Leu Lys Ala Ser Gln Val Ala Ile Gly Ile Arg Asp Asn Glu		
190 195 200		
AGG AAA GGC AGA GCT CAG CTG ATT GTG GTA GAA GAA GGG AGT GAA CCA	677	
Arg Lys Gly Arg Ala Gln Leu Ile Val Val Glu Glu Gly Ser Glu Pro		
205 210 215		
TCA GAG CTT ACA AAG GTA TTA GGG GAA AAG CCA AAG CTT AGG GAT GGA	725	
Ser Glu Leu Thr Lys Val Leu Gly Glu Lys Pro Lys Leu Arg Asp Gly		
220 225 230		
GAA GAT GAT GAT GAC ATC AAA GCA GAT ATA ACT AAT AGG AAA ATG GCT	773	
Glu Asp Asp Asp Asp Ile Lys Ala Asp Ile Thr Asn Arg Lys Met Ala		
235 240 245		
AAA CTC TAC ATG GTT TCA GAT GCC AGT GGC TCC ATG AAA GTG AGT CTG	821	
Lys Leu Tyr Met Val Ser Asp Ala Ser Gly Ser Met Lys Val Ser Leu		

250	255	260	265	
GTG GCA GAA GAA AAC CCC TTC TCC ATG GCG ATG CTT CTG TCT GAA GAA				869
Val Ala Glu Glu Asn Pro Phe Ser Met	Ala Met Leu Leu Ser Glu Glu			
270	275	280		
TGC TTC ATT TTG GAC CAC GGT GCT GCA AAA CAG ATT TTT GTA TGG AAA				917
Cys Phe Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys				
285	290	295		
GGT AAA GAT GCT AAT CCC CAG GAG AGA AAG GCT GCC ATG AAG ACA GCT				965
Gly Lys Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala				
300	305	310		
GAG GAA TTC CTA CAG CAA ATG AAT TAT TCT ACG AAT ACC CAA ATT CAA				1013
Glu Glu Phe Leu Gln Gln Met Asn Tyr Ser Thr Asn Thr Gln Ile Gln				
315	320	325		
GTT CTT CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTC TTT AAG				1061
Val Leu Pro Glu Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys				
330	335	340	345	
GAC TGG AGA GAT AGA GAT CAG AGC GAT GGC TTC GGG AAA GTG TAT GTC				1109
Asp Trp Arg Asp Arg Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val				
350	355	360		
ACA GAA AAA GTG GCT CAC GTA AAA CAA ATT CCA TTT GAT GCC TCA AAA				1157
Thr Glu Lys Val Ala His Val Lys Gln Ile Pro Phe Asp Ala Ser Lys				
365	370	375		
TTG CAC AGC TCC CCA CAA ATG GCA GCC CAG CAT CAC GTG GTG GAT GAC				1205
Leu His Ser Ser Pro Gln Met Ala Ala Gln His His Val Val Asp Asp				
380	385	390		
GGT TCT GGC AAA GTG CAG ATT TGG CGT GTA GAA AAC AAC GGT AGG GTC				1253
Gly Ser Gly Lys Val Gln Ile Trp Arg Val Glu Asn Asn Gly Arg Val				
395	400	405		
GAA ATT GAC CGA AAC TCG TAT GGT GAA TTC TAT GGT GGT GAT TGC TAC				1301
Glu Ile Asp Arg Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr				
410	415	420	425	
ATT ATA CTT TAC ACT TAT CCC AGA GGA CAG ATT ATC TAC ACC TGG CAA				1349
Ile Ile Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln				
430	435	440		
GGA GCA AAT GCC ACA CGG GAT GAG CTG ACA ACC TCC GCA TTC CTG ACT				1397
Gly Ala Asn Ala Thr Arg Asp Glu Leu Thr Ser Ala Phe Leu Thr				
445	450	455		
GTT CAG TTG GAT AGA TCC CTC GGG GGA CAG GCT GTG CAG ATT CGA GTC				1445
Val Gln Leu Asp Arg Ser Leu Gly Gly Gln Ala Val Gln Ile Arg Val				
460	465	470		
TCC CAA GGC AAA GAA CCT GCT CAC CTG CTG AGT TTG TTC AAA GAC AAA				1493
Ser Gln Gly Lys Glu Pro Ala His Leu Leu Ser Leu Phe Lys Asp Lys				
475	480	485		
CCG CTC ATT ATT TAC AAG AAC GGA ACA TCA AAG AAA GAA GGT CAG GCA				1541
Pro Leu Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Glu Gly Gln Ala				
490	495	500	505	

CCA GCC CCC CCT ATA CGC CTC TTT CAA GTC CGA AGA AAC CTG GCT TCG Pro Ala Pro Pro Ile Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser 510 515 520	1589
ATC ACC AGA ATT ATG GAG GTA GAT GTT GAT GCA AAC TCA TTG AAT TCC Ile Thr Arg Ile Met Glu Val Asp Val Asp Ala Asn Ser Leu Asn Ser 525 530 535	1637
AAT GAT GTT TTT GTC CTG AAA CTG CGA CAA AAT AAT GGC TAC ATC TGG Asn Asp Val Phe Val Leu Lys Leu Arg Gln Asn Asn Gly Tyr Ile Trp 540 545 550	1685
ATA GGA AAA GGC TCC ACA CAG GAG GAG AAA GGA GCA GAG TAC GTG Ile Gly Lys Gly Ser Thr Gln Glu Glu Lys Gly Ala Glu Tyr Val 555 560 565	1733
GCA AGC GTC CTC AAA TGC AAA ACT TCG ACG ATT CAG GAA GGC AAG GAA Ala Ser Val Leu Lys Cys Lys Thr Ser Thr Ile Gln Glu Gly Lys Glu 570 575 580 585	1781
CCA GAG GAG TTT TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC CAG ACC Pro Glu Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr Gln Thr 590 595 600	1829
TCT CCT CTG CTA GAA TCC CAG GCT GAA GAC CAT CCA CCT CGG CTT TAC Ser Pro Leu Leu Glu Ser Gln Ala Glu Asp His Pro Pro Arg Leu Tyr 605 610 615	1877
GGC TGC TCC AAC AAA ACT GGA AGA TTC ATT ATT GAA GAG GTT CCA GGA Gly Cys Ser Asn Lys Thr Gly Arg Phe Ile Ile Glu Glu Val Pro Gly 620 625 630	1925
GAG TTC ACC CAG GAT GAT TTA GCA GAA GAT GAT GTC ATG CTG TTA GAT Glu Phe Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp 635 640 645	1973
GCT TGG GAA CAG ATT TTT ATT TGG ATT GGA AAA GAT GCC AAT GAA GTT Ala Trp Glu Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn Glu Val 650 655 660 665	2021
GAG AAA TCA GAA TCT CTG AAG TCT GCC AAA ATA TAC CTT GAG ACC GAC Glu Lys Ser Glu Ser Leu Lys Ser Ala Lys Ile Tyr Leu Glu Thr Asp 670 675 680	2069
CCT TCT GGA AGA GAC AAG AGG ACG CCA ATT GTC ATC ATA AAA CAG GGT Pro Ser Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys Gln Gly 685 690 695	2117
CAT GAG CCA CCT ACT TTC ACA GGC TGG TTC CTG GGC TGG GAT TCC AGC His Glu Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp Ser Ser 700 705 710	2165
AGG TGG TAAACTGATT TTTGTAGGAA AAAAACAAAT ATAATGGGGC AGCTGTCCCA Arg Trp 715	2221
GGGGGGAAAGG AGGAGCTTGT TTAACCTTAG AAAATTAACC TCAGCCATAT GGCTATTTT CCGTGCTTAG AATTGGTTTG AAATTTCTTT TAAACTGGAA TTTTCTTATG TTAATATTTT	2281 2341

TATAACTTTT CTTATGGACC AATATTAGCT CTGCTGGATG CTGACATATC TTTATATATG	2401
ACTTTTTAAA GGGGCCG	2418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Gln Gly Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Arg	15
1 5 10	
Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val	30
20 25 30	
Pro Glu Ser Ala Tyr Gly Asn Phe Tyr Val Gly Asp Ala Tyr Leu Val	45
35 40 45	
Leu His Thr Thr Gln Ala Ser Arg Gly Phe Thr Tyr Arg Leu His Phe	60
50 55 60	
Trp Leu Gly Lys Glu Cys Thr Gln Asp Glu Ser Thr Ala Ala Ala Ile	80
65 70 75 80	
Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn	95
85 90 95	
Arg Glu Leu Gln Gly Tyr Glu Ser Thr Asp Phe Val Gly Tyr Phe Lys	110
100 105 110	
Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His	125
115 120 125	
Val Leu Thr Asn Asp Leu Thr Ala Gln Arg Leu Leu His Val Lys Gly	140
130 135 140	
Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe	160
145 150 155 160	
Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln	175
165 170 175	
Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Ser Gln	190
180 185 190	
Val Ala Ile Gly Ile Arg Asp Asn Glu Arg Lys Gly Arg Ala Gln Leu	205
195 200 205	
Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Thr Lys Val Leu	220
210 215 220	
Gly Glu Lys Pro Lys Leu Arg Asp Gly Glu Asp Asp Asp Ile Lys	240
225 230 235 240	

Ala Asp Ile Thr Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp
 245 250 255
 Ala Ser Gly Ser Met Lys Val Ser Leu Val Ala Glu Glu Asn Pro Phe
 260 265 270
 Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly
 275 280 285
 Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln
 290 295 300
 Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met
 305 310 315 320
 Asn Tyr Ser Thr Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu
 325 330 335
 Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Arg Asp Gln
 340 345 350
 Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala His Val
 355 360 365
 Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met
 370 375 380
 Ala Ala Gln His His Val Val Asp Asp Gly Ser Gly Lys Val Gln Ile
 385 390 395 400
 Trp Arg Val Glu Asn Asn Gly Arg Val Glu Ile Asp Arg Asn Ser Tyr
 405 410 415
 Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro
 420 425 430
 Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp
 435 440 445
 Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu
 450 455 460
 Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Ala
 465 470 475 480
 His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn
 485 490 495
 Gly Thr Ser Lys Lys Glu Gly Gln Ala Pro Ala Pro Pro Ile Arg Leu
 500 505 510
 Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Met Glu Val
 515 520 525
 Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Phe Val Leu Lys
 530 535 540
 Leu Arg Gln Asn Asn Gly Tyr Ile Trp Ile Gly Lys Gly Ser Thr Gln
 545 550 555 560
 Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys

565	570	575
Thr Ser Thr Ile Gln Glu Gly Lys Glu Pro Glu Glu Phe Trp Asn Ser		
580	585	590
Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Ser Gln		
595	600	605
Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly		
610	615	620
Arg Phe Ile Ile Glu Glu Val Pro Gly Glu Phe Thr Gln Asp Asp Leu		
625	630	635
Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile		
645	650	655
Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Ser Glu Ser Leu Lys		
660	665	670
Ser Ala Lys Ile Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg		
675	680	685
Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr		
690	695	700
Gly Trp Phe Leu Gly Trp Asp Ser Ser Arg Trp		
705	710	715

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2630 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 79..2223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGGTTCCCTC CTGCTGCTCT CGGTTAGTC CAAGATCAGC GATATCACGC GTCCCCCGGA	60
GCATCGCGTG CAGGAGCC ATG GCG CGG GAG CTA TAC CAC GAA GAG TTC GCC	111
Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala	
1 5 10	
CGG GCG GGC AAG CAG GCG GGG CTG CAG GTC TGG AGG ATT GAG AAG CTG	159
Arg Ala Gly Lys Gln Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu	
15 20 25	
GAG CTG GTG CCC GTG CCC CAG AGC GCT CAC GGC GAC TTC TAC GTC GGG	207
Glu Leu Val Pro Val Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly	
30 35 40	

GAT	GCC	TAC	CTG	GTG	CTG	CAC	ACG	GCC	AAG	ACG	AGC	CGA	GGC	TTC	ACC	255
Asp	Ala	Tyr	Leu	Val	Leu	His	Thr	Ala	Lys	Thr	Ser	Arg	Gly	Phe	Thr	
45					50					55						
TAC	CAC	CTG	CAC	TTC	TGG	CTC	GGA	AAG	GAG	TGT	TCC	CAG	GAT	GAA	AGC	303
Tyr	His	Leu	His	Phe	Trp	Leu	Gly	Lys	Glu	Cys	Ser	Gln	Asp	Glu	Ser	
60					65					70					75	
ACA	GCT	GCT	GCC	ATC	TTC	ACT	GTT	CAG	ATG	GAT	GAC	TAT	TTG	GGT	GGC	351
Thr	Ala	Ala	Ala	Ile	Phe	Thr	Val	Gln	Met	Asp	Asp	Tyr	Leu	Gly	Gly	
								80		85				90		
AAG	CCA	GTG	CAG	AAT	AGA	GAA	CTT	CAA	GGA	TAT	GAG	TCT	AAT	GAC	TTT	399
Lys	Pro	Val	Gln	Asn	Arg	Glu	Leu	Gln	Gly	Tyr	Glu	Ser	Asn	Asp	Phe	
								95		100				105		
GTT	AGC	TAT	TTC	AAA	GGC	GGT	CTG	AAA	TAC	AAG	GCT	GGA	GGC	GTG	GCA	447
Val	Ser	Tyr	Phe	Lys	Gly	Gly	Leu	Lys	Tyr	Lys	Ala	Gly	Gly	Val	Ala	
								110		115				120		
TCT	GGA	TTA	AAT	CAT	GTT	CTT	ACG	AAC	GAC	CTG	ACA	GCC	AAG	AGG	CTC	495
Ser	Gly	Leu	Asn	His	Val	Leu	Thr	Asn	Asp	Leu	Thr	Ala	Lys	Arg	Leu	
								125		130				135		
CTA	CAT	GTG	AAG	GGT	CGT	AGA	GTG	GTG	AGA	GCC	ACA	GAA	GTT	CCC	CTT	543
Leu	His	Val	Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Leu	
								140		145				150		
AGC	TGG	GAC	AGT	TTC	AAC	AAG	GGT	GAC	TGC	TTC	ATC	ATT	GAC	CTT	GGC	591
Ser	Trp	Asp	Ser	Phe	Asn	Lys	Gly	Asp	Cys	Phe	Ile	Ile	Asp	Leu	Gly	
								160		165				170		
ACC	GAA	ATT	TAT	CAG	TGG	TGT	GGT	TCC	TCG	TGC	AAC	AAA	TAT	GAA	CGT	639
Thr	Glu	Ile	Tyr	Gln	Trp	Cys	Gly	Ser	Ser	Cys	Asn	Lys	Tyr	Glu	Arg	
								175		180				185		
CTG	AAG	GCA	AAC	CAG	GTA	GCT	ACT	GGC	ATT	CGG	TAC	AAT	GAA	AGG	AAA	687
Leu	Lys	Ala	Asn	Gln	Val	Ala	Thr	Gly	Ile	Arg	Tyr	Asn	Glu	Arg	Lys	
								190		195				200		
GGA	AGG	TCT	GAA	CTA	ATT	GTC	GTG	GAA	GGA	AGT	GAA	CCC	TCA	GAA	735	
Gly	Arg	Ser	Glu	Leu	Ile	Val	Val	Glu	Glu	Gly	Ser	Glu	Pro	Ser	Glu	
								205		210				215		
CTT	ATA	AAG	GTC	TTA	GGG	GAA	AAG	CCA	GAG	CTT	CCA	GAT	GGA	GGT	GAT	783
Leu	Ile	Lys	Val	Leu	Gly	Glu	Lys	Pro	Glu	Leu	Pro	Asp	Gly	Gly	Asp	
								220		225				230		
GAT	GAT	GAC	ATT	ATA	GCA	GAC	ATA	AGT	AAC	AGG	AAA	ATG	GCT	AAA	CTA	831
Asp	Asp	Asp	Ile	Ile	Ala	Asp	Ile	Ser	Asn	Arg	Lys	Met	Ala	Lys	Leu	
								240		245				250		
TAC	ATG	GTT	TCA	GAT	GCA	AGT	GGC	TCC	ATG	AGA	GTG	ACT	GTG	GTG	GCA	879
Tyr	Met	Val	Ser	Asp	Ala	Ser	Gly	Ser	Met	Arg	Val	Thr	Val	Val	Ala	
								255		260				265		
GAA	GAA	AAC	CCC	TTC	TCA	ATG	GCA	ATG	CTG	CTG	TCT	GAA	GAA	TGC	TTT	927
Glu	Glu	Asn	Pro	Phe	Ser	Met	Ala	Met	Leu	Leu	Ser	Glu	Glu	Cys	Phe	
								270		275				280		

ATT TTG GAC CAC GGG GCT GCC AAA CAA ATT TTC GTA TGG AAA GGT AAA Ile Leu Asp His Gly Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys 285 290 295	975
GAT GCT AAT CCC CAA GAG AGG AAG GCT GCA ATG AAG ACA GCT GAA GAA Asp Ala Asn Pro Gln Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu 300 305 310 315	1023
TTT CTA CAG CAA ATG AAT TAT TCC AAG AAT ACC CAA ATT CAA GTT CTT Phe Leu Gln Gln Met Asn Tyr Ser Lys Asn Thr Gln Ile Gln Val Leu 320 325 330	1071
CCA GAA GGA GGT GAA ACA CCA ATC TTC AAA CAG TTT TTT AAG GAC TGG Pro Glu Gly Gly Glu Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp 335 340 345	1119
AGA GAT AAA GAT CAG AGT GAT GGC TTC GGG AAA GTT TAT GTC ACA GAG Arg Asp Lys Asp Gln Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu 350 355 360	1167
AAA GTG GCT CAA ATA AAA CAA ATT CCC TTT GAT GCC TCA AAA TTA CAC Lys Val Ala Gln Ile Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His 365 370 375	1215
AGT TCT CCG CAG ATG GCA GCC CAG CAC AAT ATG GTG GAT GAT GGT TCT Ser Ser Pro Gln Met Ala Ala Gln His Asn Met Val Asp Asp Gly Ser 380 385 390 395	1263
GGC AAA GTG GAG ATT TGG CGT GTA GAA AAC AAT GGT AGG ATC CAA GTT Gly Lys Val Glu Ile Trp Arg Val Glu Asn Asn Gly Arg Ile Gln Val 400 405 410	1311
GAC CAA AAC TCA TAT GGT GAA TTC TAT GGT GGT GAC TGC TAC ATC ATA Asp Gln Asn Ser Tyr Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile 415 420 425	1359
CTC TAC ACC TAT CCC AGA GGA CAG ATT ATC TAC ACG TGG CAA GGA GCA Leu Tyr Thr Tyr Pro Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala 430 435 440	1407
AAT GCC ACA CGA GAT GAG CTG ACA ACA TCT GCG TTC CTG ACT GTT CAG Asn Ala Thr Arg Asp Glu Leu Thr Ser Ala Phe Leu Thr Val Gln 445 450 455	1455
TTG GAT CGG TCC CTT GGA GGA CAG GCT GTG CAG ATC CGA GTC TCC CAA Leu Asp Arg Ser Leu Gly Gln Ala Val Gln Ile Arg Val Ser Gln 460 465 470 475	1503
GGC AAA GAG CCT GTT CAC CTA CTG AGT TTG TTC AAA GAC AAA CCG CTC Gly Lys Glu Pro Val His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu 480 485 490	1551
ATT ATT TAC AAG AAT GGA ACA TCA AAG AAA GGA GGT CAG GCA CCT GCT Ile Ile Tyr Lys Asn Gly Thr Ser Lys Lys Gly Gly Gln Ala Pro Ala 495 500 505	1599
CCC CCT ACA CGC CTC TTT CAA GTC CGG AGA AAC CTG GCA TCT ATC ACC Pro Pro Thr Arg Leu Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr 510 515 520	1647
AGA ATT GTG GAG GTT GAT GCA AAT TCA CTG AAT TCT AAC GAT	1695

Arg Ile Val Glu Val Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp	535	
525	530	
GTT TGT GTC CTG AAA CTG CCA CAA AAT AGT GGC TAC ATC TGG GTA GGA		1743
Val Cys Val Leu Lys Leu Pro Gln Asn Ser Gly Tyr Ile Trp Val Gly		
540	545	555
AAA GGT GCT AGC CAG GAG GAG AAA GGA GCA GAG TAT GTA GCA AGT		1791
Lys Gly Ala Ser Gln Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser		
560	565	570
GTC CTA AAG TGC AAA ACC TTA AGG ATC CAA GAA GGC GAG GAG CCA GAG		1839
Val Leu Lys Cys Lys Thr Leu Arg Ile Gln Glu Gly Glu Pro Glu		
575	580	585
GAG TTC TGG AAT TCC CTT GGA GGG AAA AAA GAC TAC CAG ACC TCA CCA		1887
Glu Phe Trp Asn Ser Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro		
590	595	600
CTA CTG GAA ACC CAG GCT GAA GAC CAT CCA CCT CGG CTT TAC GGC TGC		1935
Leu Leu Glu Thr Gln Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys		
605	610	615
TCT AAC AAA ACT GGA AGA TTT GTT ATT GAA GAG ATT CCA GGA GAG TTC		1983
Ser Asn Lys Thr Gly Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe		
620	625	630
ACC CAG GAT GAT TTA GCT GAA GAT GAT GTC ATG TTA CTA GAT GCT TGG		2031
Thr Gln Asp Asp Leu Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp		
640	645	650
GAA CAG ATA TTT ATT TGG ATT GGC AAA GAT GCT AAT GAA GTT GAG AAA		2079
Glu. Gln Ile Phe Ile Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys		
655	660	665
AAA GAA TCT CTG AAG TCT GCC AAA ATG TAC CTT GAG ACA GAC CCT TCT		2127
Lys Glu Ser Leu Lys Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser		
670	675	680
GGA AGA GAC AAG AGG ACA CCA ATT GTC ATC ATA AAA CAG GGC CAT GAG		2175
Gly Arg Asp Lys Arg Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu		
685	690	695
CCA CCC ACA TTC ACA GGC TGG TTC CTG GGC TGG GAT TCC AGC AAG TGG		2223
Pro Pro Thr Phe Thr Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp		
700	705	710
TAAATTGGTA TTTGTAAAAA GCAAACAAAC ATTACAAGGC AGTTATCTCA TTGCTGTTT		2283
GGGAGAGGAA CGGGAAAAGC TTTTGCTTA TTTGTCTTT GAAAATTAAG GCTGGGCGCG		2343
GTGGCTCACA CCTGTAATCC CAGCACTTG AGAGGATGAG GTAGGCAGGAT CACTGGGGTC		2403
AGGATTCGA GACCAGCCTG GCCAACATGG CGAACACCTCG CCTCTACTAA AAATACAAAA		2463
AAATTAGCTG CGCGTGGTGG TGCACGCCTG TAGTCCCTGC TACTTGGAAAG GCTGAGACAG		2523
GAAAATTGCT TGAGCCCAGG AGGCTGAGGT TGCAGTGAGC CAGGATTGCG CCACCCACACT		2583
CCAGCCTGGG CAACAGAGAC TCTGTCTCAA AAAAAAAA AAAAAAA		2630

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 715 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Arg Glu Leu Tyr His Glu Glu Phe Ala Arg Ala Gly Lys Gln
1 5 10 15

Ala Gly Leu Gln Val Trp Arg Ile Glu Lys Leu Glu Leu Val Pro Val
20 25 30

Pro Gln Ser Ala His Gly Asp Phe Tyr Val Gly Asp Ala Tyr Leu Val
35 40 45

Leu His Thr Ala Lys Thr Ser Arg Gly Phe Thr Tyr His Leu His Phe
50 55 60

Trp Leu Gly Lys Glu Cys Ser Gln Asp Glu Ser Thr Ala Ala Ala Ile
65 70 75 80

Phe Thr Val Gln Met Asp Asp Tyr Leu Gly Gly Lys Pro Val Gln Asn
85 90 95

Arg Glu Leu Gln Gly Tyr Glu Ser Asn Asp Phe Val Ser Tyr Phe Lys
100 105 110

Gly Gly Leu Lys Tyr Lys Ala Gly Gly Val Ala Ser Gly Leu Asn His
115 120 125

Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His Val Lys Gly
130 135 140

Arg Arg Val Val Arg Ala Thr Glu Val Pro Leu Ser Trp Asp Ser Phe
145 150 155 160

Asn Lys Gly Asp Cys Phe Ile Ile Asp Leu Gly Thr Glu Ile Tyr Gln
165 170 175

Trp Cys Gly Ser Ser Cys Asn Lys Tyr Glu Arg Leu Lys Ala Asn Gln
180 185 190

Val Ala Thr Gly Ile Arg Tyr Asn Glu Arg Lys Gly Arg Ser Glu Leu
195 200 205

Ile Val Val Glu Glu Gly Ser Glu Pro Ser Glu Leu Ile Lys Val Leu
210 215 220

Gly Glu Lys Pro Glu Leu Pro Asp Gly Gly Asp Asp Asp Asp Ile Ile
225 230 235 240

Ala Asp Ile Ser Asn Arg Lys Met Ala Lys Leu Tyr Met Val Ser Asp
245 250 255

Ala Ser Gly Ser Met Arg Val Thr Val Val Ala Glu Glu Asn Pro Phe

260	265	270
Ser Met Ala Met Leu Leu Ser Glu Glu Cys Phe Ile Leu Asp His Gly		
275	280	285
Ala Ala Lys Gln Ile Phe Val Trp Lys Gly Lys Asp Ala Asn Pro Gln		
290	295	300
Glu Arg Lys Ala Ala Met Lys Thr Ala Glu Glu Phe Leu Gln Gln Met		
305	310	315
Asn Tyr Ser Lys Asn Thr Gln Ile Gln Val Leu Pro Glu Gly Gly Glu		
325	330	335
Thr Pro Ile Phe Lys Gln Phe Phe Lys Asp Trp Arg Asp Lys Asp Gln		
340	345	350
Ser Asp Gly Phe Gly Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile		
355	360	365
Lys Gln Ile Pro Phe Asp Ala Ser Lys Leu His Ser Ser Pro Gln Met		
370	375	380
Ala Ala Gln His Asn Met Val Asp Asp Gly Ser Gly Lys Val Glu Ile		
385	390	395
Trp Arg Val Glu Asn Asn Gly Arg Ile Gln Val Asp Gln Asn Ser Tyr		
405	410	415
Gly Glu Phe Tyr Gly Gly Asp Cys Tyr Ile Ile Leu Tyr Thr Tyr Pro		
420	425	430
Arg Gly Gln Ile Ile Tyr Thr Trp Gln Gly Ala Asn Ala Thr Arg Asp		
435	440	445
Glu Leu Thr Thr Ser Ala Phe Leu Thr Val Gln Leu Asp Arg Ser Leu		
450	455	460
Gly Gly Gln Ala Val Gln Ile Arg Val Ser Gln Gly Lys Glu Pro Val		
465	470	475
His Leu Leu Ser Leu Phe Lys Asp Lys Pro Leu Ile Ile Tyr Lys Asn		
485	490	495
Gly Thr Ser Lys Lys Gly Gly Gln Ala Pro Ala Pro Pro Thr Arg Leu		
500	505	510
Phe Gln Val Arg Arg Asn Leu Ala Ser Ile Thr Arg Ile Val Glu Val		
515	520	525
Asp Val Asp Ala Asn Ser Leu Asn Ser Asn Asp Val Cys Val Leu Lys		
530	535	540
Leu Pro Gln Asn Ser Gly Tyr Ile Trp Val Gly Lys Gly Ala Ser Gln		
545	550	555
Glu Glu Glu Lys Gly Ala Glu Tyr Val Ala Ser Val Leu Lys Cys Lys		
565	570	575
Thr Leu Arg Ile Gln Glu Gly Glu Glu Pro Glu Glu Phe Trp Asn Ser		
580	585	590

Leu Gly Gly Lys Lys Asp Tyr Gln Thr Ser Pro Leu Leu Glu Thr Gln
 595 600 605
 Ala Glu Asp His Pro Pro Arg Leu Tyr Gly Cys Ser Asn Lys Thr Gly
 610 615 620
 Arg Phe Val Ile Glu Glu Ile Pro Gly Glu Phe Thr Gln Asp Asp Leu
 625 630 635 640
 Ala Glu Asp Asp Val Met Leu Leu Asp Ala Trp Glu Gln Ile Phe Ile
 645 650 655
 Trp Ile Gly Lys Asp Ala Asn Glu Val Glu Lys Lys Glu Ser Leu Lys
 660 665 670
 Ser Ala Lys Met Tyr Leu Glu Thr Asp Pro Ser Gly Arg Asp Lys Arg
 675 680 685
 Thr Pro Ile Val Ile Ile Lys Gln Gly His Glu Pro Pro Thr Phe Thr
 690 695 700
 Gly Trp Phe Leu Gly Trp Asp Ser Ser Lys Trp
 705 710 715

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu Asn His Val Leu Thr Asn Asp Leu Thr Ala Lys Arg Leu Leu His
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Val Tyr Val Thr Glu Lys Val Ala Gln Ile Lys Gln Ile Pro Phe

1

5

10

15

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 782 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Pro	His	Arg	Pro	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Leu	Ser	Leu
1									10					15	
Ala	Leu	Cys	Ala	Leu	Ser	Leu	Pro	Val	Arg	Ala	Ala	Thr	Ala	Ser	Arg
								20	25			30			
Gly	Ala	Ser	Gln	Ala	Gly	Ala	Pro	Gln	Gly	Arg	Val	Pro	Glu	Ala	Arg
								35	40			45			
Pro	Asn	Ser	Met	Val	Val	Glu	His	Pro	Glu	Phe	Leu	Lys	Ala	Gly	Lys
						55					60				
Glu	Pro	Gly	Leu	Gln	Ile	Trp	Arg	Val	Glu	Lys	Phe	Asp	Leu	Val	Pro
						65	70		75			80			
Val	Pro	Thr	Asn	Leu	Tyr	Gly	Asp	Phe	Phe	Thr	Gly	Asp	Ala	Tyr	Val
						85		90				95			
Ile	Leu	Lys	Thr	Val	Gln	Leu	Arg	Asn	Gly	Asn	Leu	Gln	Tyr	Asp	Leu
						100		105				110			
His	Tyr	Trp	Leu	Gly	Asn	Glu	Cys	Ser	Gln	Asp	Glu	Ser	Gly	Ala	Ala
						115		120				125			
Ala	Ile	Phe	Thr	Val	Gln	Leu	Asp	Asp	Tyr	Leu	Asn	Gly	Arg	Ala	Val
						130		135			140				
Gln	His	Arg	Glu	Val	Gln	Gly	Phe	Glu	Ser	Ala	Thr	Phe	Leu	Gly	Tyr
						145		150			155			160	
Phe	Lys	Ser	Gly	Leu	Lys	Tyr	Lys	Lys	Gly	Gly	Val	Ala	Ser	Gly	Phe
						165		170				175			
Lys	His	Val	Val	Pro	Asn	Glu	Val	Val	Val	Gln	Arg	Leu	Phe	Gln	Val
						180		185			190				
Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Val	Ser	Trp	Glu
						195		200			205				
Ser	Phe	Asn	Asn	Gly	Asp	Cys	Phe	Ile	Leu	Asp	Leu	Gly	Asn	Asn	Ile
						210		215			220				
His	Gln	Trp	Cys	Gly	Ser	Asn	Ser	Asn	Arg	Tyr	Glu	Arg	Leu	Lys	Ala
						225		230			235			240	

Thr Gln Val Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala
 245 250 255
 Arg Val His Val Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln
 260 265 270
 Val Leu Gly Pro Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala
 275 280 285
 Lys Glu Asp Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser
 290 295 300
 Asn Gly Ala Gly Thr Met Ser Val Leu Val Ala Asp Glu Asn Pro
 305 310 320
 Phe Ala Gln Gly Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His
 325 330 335
 Gly Lys Asp Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr
 340 345 350
 Glu Glu Arg Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys
 355 360 365
 Met Asp Tyr Pro Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly
 370 375 380
 Glu Thr Pro Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp
 385 390 395 400
 Gln Thr Asp Gly Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn
 405 410 415
 Val Glu Arg Val Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala
 420 425 430
 Met Ala Ala Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln
 435 440 445
 Ile Trp Arg Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr
 450 455 460
 Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
 465 470 475 480
 Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
 485 490 495
 Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
 500 505 510
 Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
 515 520 525
 Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
 530 535 540
 Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
 545 550 555 560

Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
 565 570 575
 Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
 580 585 590
 Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
 595 600 605
 Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
 610 615 620
 Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
 625 630 635 640
 Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
 645 650 655
 Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
 660 665 670
 Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
 675 680 685
 Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
 690 695 700
 Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Lys
 705 710 715 720
 Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
 725 730 735
 Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
 740 745 750
 Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
 755 760 765
 Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
 770 775 780

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 827 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Thr Lys Leu Ser Ala Gln Val Lys Gly Ser Leu Asn Ile Thr Thr
 1 5 10 15
 Pro Gly Leu Gln Ile Trp Arg Ile Glu Ala Met Gln Met Val Pro Val

20	25	30	
Pro Ser Ser Thr Phe Gly Ser Phe Phe Asp Gly Asp Cys Tyr Ile Ile			
35	40	45	
Leu Ala Ile His Lys Thr Ala Ser Ser Leu Ser Tyr Asp Ile His Tyr			
50	55	60	
Trp Ile Gly Gln Asp Ser Ser Leu Asp Glu Gln Gly Ala Ala Ala Ile			
65	70	75	80
Tyr Thr Thr Gln Met Asp Asp Phe Leu Lys Gly Arg Ala Val Gln His			
85	90	95	
Arg Glu Val Gln Gly Asn Glu Ser Glu Ala Phe Arg Gly Tyr Phe Lys			
100	105	110	
Gln Gly Leu Val Ile Arg Lys Gly Gly Val Ala Ser Gly Met Lys His			
115	120	125	
Val Glu Thr Asn Ser Tyr Asp Val Gln Arg Leu Leu His Val Lys Gly			
130	135	140	
Lys Arg Asn Val Val Ala Gly Glu Val Glu Met Ser Trp Lys Ser Phe			
145	150	155	160
Asn Arg Gly Asp Val Phe Leu Leu Asp Leu Gly Lys Leu Ile Ile Gln			
165	170	175	
Trp Asn Gly Pro Glu Ser Thr Arg Met Glu Arg Leu Arg Gly Met Thr			
180	185	190	
Leu Ala Lys Glu Ile Arg Asp Gln Glu Arg Gly Arg Thr Tyr Val			
195	200	205	
Gly Val Val Asp Gly Glu Asn Glu Leu Ala Ser Pro Lys Leu Met Glu			
210	215	220	
Val Met Asn His Val Leu Gly Lys Arg Arg Glu Leu Lys Ala Ala Val			
225	230	235	240
Pro Asp Thr Val Val Glu Pro Ala Leu Lys Ala Ala Leu Lys Leu Tyr			
245	250	255	
His Val Ser Asp Ser Glu Gly Asn Leu Val Val Arg Glu Val Ala Thr			
260	265	270	
Arg Pro Leu Thr Gln Asp Leu Leu Ser His Glu Asp Cys Tyr Ile Leu			
275	280	285	
Asp Gln Gly Gly Leu Lys Ile Tyr Val Trp Lys Gly Lys Lys Ala Asn			
290	295	300	
Glu Gln Glu Lys Lys Gly Ala Met Ser His Ala Leu Asn Phe Ile Lys			
305	310	315	320
Ala Lys Gln Tyr Pro Pro Ser Thr Gln Val Glu Val Gln Asn Asp Gly			
325	330	335	
Ala Glu Ser Ala Val Phe Gln Gln Leu Phe Gln Lys Trp Thr Ala Ser			
340	345	350	

Asn Arg Thr Ser Gly Leu Gly Lys Thr His Thr Val Gly Ser Val Ala
 355 360 365
 Lys Val Glu Gln Val Lys Phe Asp Ala Thr Ser Met His Val Lys Pro
 370 375 380 385
 Gln Val Ala Ala Gln Gln Lys Met Val Asp Asp Gly Ser Gly Glu Val
 390 395 400
 Gln Val Trp Arg Ile Glu Asn Leu Glu Leu Val Pro Val Asp Ser Lys
 405 410 415
 Trp Leu Gly His Phe Tyr Gly Asp Cys Tyr Leu Leu Leu Tyr Thr
 420 425 430
 Tyr Leu Ile Gly Glu Lys Gln His Tyr Leu Leu Tyr Val Trp Gln Gly
 435 440 445
 Ser Gln Ala Ser Gln Asp Glu Ile Thr Ala Ser Ala Tyr Gln Ala Val
 450 455 460
 Ile Leu Asp Gln Lys Tyr Asn Gly Glu Pro Val Gln Ile Arg Val Pro
 465 470 475 480
 Met Gly Lys Glu Pro Pro His Leu Met Ser Ile Phe Lys Gly Arg Met
 485 490 495
 Val Val Tyr Gln Gly Gly Thr Ser Arg Thr Asn Asn Leu Glu Thr Gly
 500 505 510
 Pro Ser Thr Arg Leu Phe Gln Val Gln Gly Thr Gly Ala Asn Asn Thr
 515 520 525
 Lys Ala Phe Glu Val Pro Ala Arg Ala Asn Phe Leu Asn Ser Asn Asp
 530 535 540
 Val Phe Val Leu Lys Thr Gln Ser Cys Cys Tyr Leu Trp Cys Gly Lys
 545 550 555 560
 Gly Cys Ser Gly Asp Glu Arg Glu Met Ala Lys Met Val Ala Asp Thr
 565 570 575
 Ile Ser Arg Thr Glu Lys Gln Val Val Val Glu Gly Gln Glu Pro Ala
 580 585 590
 Asn Phe Trp Met Ala Leu Gly Gly Lys Ala Pro Tyr Ala Asn Thr Lys
 595 600 605
 Arg Leu Gln Glu Glu Asn Leu Val Ile Thr Pro Arg Leu Phe Glu Cys
 610 615 620
 Ser Asn Lys Thr Gly Arg Phe Leu Ala Thr Glu Ile Pro Asp Phe Asn
 625 630 635 640
 Gln Asp Asp Leu Glu Glu Asp Asp Val Phe Leu Leu Asp Val Trp Asp
 645 650 655
 Gln Val Phe Phe Trp Ile Gly Lys His Ala Asn Glu Glu Glu Lys Lys
 660 665 670

Ala Ala Ala Thr Thr Ala Gln Glu Tyr Leu Lys Thr His Pro Ser Gly
 675 680 685
 Arg Asp Pro Glu Thr Pro Ile Ile Val Val Lys Gln Gly His Glu Pro
 690 695 700
 Pro Thr Phe Thr Gly Trp Phe Leu Ala Trp Asp Pro Phe Lys Trp Ser
 705 710 715 720
 Asn Thr Lys Ser Tyr Glu Asp Leu Lys Ala Glu Ser Gly Asn Leu Arg
 725 730 735
 Asp Trp Ser Gln Ile Thr Ala Glu Val Thr Ser Pro Lys Val Asp Val
 740 745 750
 Phe Asn Ala Asn Ser Asn Leu Ser Ser Gly Pro Leu Pro Ile Phe Pro
 755 760 765
 Leu Glu Gln Leu Val Asn Lys Pro Val Glu Glu Leu Pro Glu Gly Val
 770 775 780
 Asp Pro Ser Arg Lys Glu Glu His Leu Ser Ile Glu Asp Phe Thr Gln
 785 790 795 800
 Ala Phe Gly Met Thr Pro Ala Ala Phe Ser Ala Leu Pro Arg Trp Lys
 805 810 815
 Gln Gln Asn Leu Lys Lys Glu Lys Gly Leu Phe
 820 825

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GATGCGGATC CAAYGAYYTN ACNGCNCA

28

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATGCATCGA TACRTGNGCN ACYTTYTC

28

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCGAGGGTG GCGACGACTC C

21

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCGGCCGCTT GACACCAGAC CAA

23

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CAGCTATGAC CATGATTACG CCAA

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "PRIMER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACGACGGCCA GTGAATTGCG TAAT

24

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Lys Val Ala Lys Val Glu Gln Val Lys Phe Asp Ala
1 5 10